

IN THE SPECIFICATION:

Please amend the paragraph beginning on page 1, line 5 as follows:

--CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation of application Serial Number 09/051,843, which is a 371 application filed on June 29, 1998 based on PCT/AU96/00668, filed October 23, 1996.--

Please amend the paragraph beginning on page 37, line 3 as follows:

A library was constructed in λ ZAP II using *ApoI* digested genomic DNA from embryonal stem cells and screened with a pool of ^{32}P -labelled oligonucleotides encoding the amino acid sequence Trp-Ser-Asp-Trp-Ser found in many members of the haemopoietin receptor family. One hybridizing bacteriophage clone was found to contain a sequence that appeared to encode part of a novel member of the haemopoietin receptor family. This receptor was given the operational name NR4. The sequence of the genomic clone was used to isolate cDNAs encoding NR4 from WEHI-3B cell, peritoneal macrophage, bone marrow, skin and kidney libraries. A composite of the nucleotide sequence ~~{SEQ ID NO:1}~~(SEQ ID NO:1) and predicted amino acid sequence ~~{SEQ ID NO:2}~~(SEQ ID NO:2) of these cDNAs is shown in Figure 1. The NR4 cDNA is predicted to encode for a protein of 424 amino acid residues, containing a putative signal sequence and transmembrane domain. The extracellular region of the protein contained an immunoglobulin-like domain (amino acids 27-117), in addition to a typical haemopoietin receptor domain (amino acids 118-340) which includes four conserved cysteine residues and the characteristic Trp-Ser-Asp-Trp-Ser motif (SEQ ID NO:9) (Figure 1; in bold as WSXWS). The cytoplasmic tail of the new receptor was 60 amino acids in length.